#4

SEQUENCE LISTING

<110>  ZHU, JIAN-KANG

LIU, JIPING

ISHITANI, MANABU

HALFTER, URSULA

KIM, CHEOL-SOO

<120>  PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS

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<140>  09/824,735

<141>  2001-04-04

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<151>  2000-04-04

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| cgggaaaatc | acggatttat | gttttttggt | ggaaaaatta | cgagtttact | ttttctcaat | 180 |
| ttcattgctt | gtatatttaa | gaaatttgga | aaaatattaa | ttttattaaa | ttggtttaga | 240 |
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ttgtagttaa aaatagaaaa ttttactaat ttgagttcga ttaatcatag tctagataat    1320

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Tyr Glu Val Gly Arg Thr Ile Gly Glu Gly Thr Phe Ala Lys Val Lys
             15                  20                  25

ttt gcg agg aac aca gac act ggt gat aat gta gcc atc aaa att atg    2129
Phe Ala Arg Asn Thr Asp Thr Gly Asp Asn Val Ala Ile Lys Ile Met
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Ala Lys Ser Thr Ile Leu Lys Asn Arg Met Val Asp Gln
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gattgttttt tacatggaaa ctaaggttgt tgcgtcaatg gtatgatctt tgatttcgtt    2238

taaagctctt ttacag ata aaa aga gag ata tct ata atg aag att gtt cgt    2290
               Ile Lys Arg Glu Ile Ser Ile Met Lys Ile Val Arg
                             60                  65

cac ccg aac ata gtg agg ttg tat gag gtatgtttgt ttgtttccat           2337
His Pro Asn Ile Val Arg Leu Tyr Glu
        70                  75

gcatctgcga aattttatct ctgaagtgtt tttgcatcat tgttcttctg ttgttttttt    2397

gtgatttttcc cgatgtag gtg ttg gcg agt cct tcg aaa ata tat ata gtt     2448
                    Val Leu Ala Ser Pro Ser Lys Ile Tyr Ile Val
                                 80                  85

ttg gag ttt gtg aca gga gga gag ctc ttt gat aga att gtacggaact      2497
Leu Glu Phe Val Thr Gly Gly Glu Leu Phe Asp Arg Ile
        90                  95                  100

tgcatacttg taggcagcgt ccattagtta aaacctctct acttaatttt ttaatatatg    2557

aaatctttca tgcag gtt cat aaa ggg agg ctt gaa gaa agt gag tct cgg    2608
              Val His Lys Gly Arg Leu Glu Glu Ser Glu Ser Arg
                             105                  110

aaa tac ttt caa cag ctt gta gat gct gtt gct cat tgt cac tgc aag    2656
Lys Tyr Phe Gln Gln Leu Val Asp Ala Val Ala His Cys His Cys Lys
        115                  120                  125

ggt gtt tac cac cgt gac cta aag gtaaagacgt gttttgttt accaatattc     2710
Gly Val Tyr His Arg Asp Leu Lys
        130                  135

ctcagaatat ctcactgcgt tgcaatccag acttgatatt tttgtgtcgc tatgttatgt    2770

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            Pro Glu Asn Leu Leu Leu Asp Thr Asn Gly Asn Leu Lys Val
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tcg gat ttc gga ctc agt gca ttg cct cag gaa gtaagtgctc ttatctctgc   2872
Ser Asp Phe Gly Leu Ser Ala Leu Pro Gln Glu
        155                  160

ttcagcagtc tgcttacgtg gtcattaact tgttatatac tcaatcag gga gta gaa    2929
                                                        Gly Val Glu
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ctt ctg cgt acc aca tgt gga act ccg aac tat gta gct cca gag gta      2977
Leu Leu Arg Thr Thr Cys Gly Thr Pro Asn Tyr Val Ala Pro Glu Val
165             170             175             180

ctt agt gga cag ggt tac gat ggt tca gca gct gat att tgg tct tgc      3025
Leu Ser Gly Gln Gly Tyr Asp Gly Ser Ala Ala Asp Ile Trp Ser Cys
            185             190             195

ggg gtt att ctt ttc gtt ata ttg gct gga tat tta cct ttt tcc gag      3073
Gly Val Ile Leu Phe Val Ile Leu Ala Gly Tyr Leu Pro Phe Ser Glu
            200             205             210

acg gat ctt cca ggg ttg tac aga aaa gtaagtaaca tatctttcgg            3120
Thr Asp Leu Pro Gly Leu Tyr Arg Lys
            215             220

gaagaaatca tgaattcctt gtcatggctt ttgtcaaacc gtttattgat ttggttttgc    3180

aatttcaccc ttagttttga cttttacac attgttattt acag ata aat gca gca      3236
                                                 Ile Asn Ala Ala
                                                              225

gag ttt tct tgt cca ccg tgg ttt tcc gca gaa gtg aag ttt tta ata      3284
Glu Phe Ser Cys Pro Pro Trp Phe Ser Ala Glu Val Lys Phe Leu Ile
            230             235             240

cat agg ata ctt gac ccc aat ccc aaa aca gtgagtattt tgctttgttc        3334
His Arg Ile Leu Asp Pro Asn Pro Lys Thr
            245             250

tctcctagct atcaggtttt ggtgatattt aatgttctag taattatatc tgtttatcta    3394

ttattgtttc tcaattagag cag cgt att caa att caa gga atc aag aaa gat    3447
                       Arg Ile Gln Ile Gln Gly Ile Lys Lys Asp
                                       255             260

cct tgg ttc aga tta aat tat gtg cct ata cga gca agg gaa gaa gaa      3495
Pro Trp Phe Arg Leu Asn Tyr Val Pro Ile Arg Ala Arg Glu Glu Glu
            265             270             275

gaa gtg aat ttg gat gat att cgt gca gtt ttt gat gga att gag          3540
Glu Val Asn Leu Asp Asp Ile Arg Ala Val Phe Asp Gly Ile Glu
            280             285             290

gtttgtgctt cgccttcatt atatgctctt tgctggtcaa ttccatttaa atgttaagat    3600

ctcttaggaa cgtttggatg accaagaaga agtgtttgct acaggataga acaaaatagt    3660

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ttgttaaact aaaacctcag tatctgtctt agctaaagtt acttttactt gtttttcatt      4020

aagttgacct gtcaattgca cttgttcaca g ggc agt tat gta gcg gag aat        4072
                                   Gly Ser Tyr Val Ala Glu Asn
                                                   295

gta gag aga aat gat gaa ggg ccc ctg atg atg aat gcc ttt gag atg      4120
Val Glu Arg Asn Asp Glu Gly Pro Leu Met Met Asn Ala Phe Glu Met
300                         305             310                 315

att acc tta tca caa ggc tta aat tta tct gca cta ttt gac agg cga      4168
Ile Thr Leu Ser Gln Gly Leu Asn Leu Ser Ala Leu Phe Asp Arg Arg
                    320             325                 330

cag gtagtacctg attttctatt actggtcata gagatctcca tttcgaataa          4221
Gln

aagaatgtcg gtagcatcta ttcttcagac tgcccgtttt gactgcctta tgatgctgtg      4281

ttcttagttt gttataataa ctataagttc attagatgat tggttgcatg cattagtag       4341

atacaaatgg aatccaaaat gttcctgcat attgatggct gatcctttga tctcgcag        4399

gat ttt gtt aaa agg caa acc cgt ttt gtt tct cga agg gaa cct agt      4447
Asp Phe Val Lys Arg Gln Thr Arg Phe Val Ser Arg Arg Glu Pro Ser
        335                 340                 345

gag ata att gct aac att gag gct gta gcg aac tca atg ggt ttt aag      4495
Glu Ile Ile Ala Asn Ile Glu Ala Val Ala Asn Ser Met Gly Phe Lys
    350                 355                 360

tct cat aca cga aac ttc aag gtaacgaatt cctagcatat tacacttatc         4546
Ser His Thr Arg Asn Phe Lys
365                 370

acagagatta tgcattattt taaaactctc aactgttaaa cgcatgtgta gatagattga      4606

taagattgac aaggaaactt agtttatatc tctggcgttc aaaaacgaaa gtcctagtgt      4666

gaattatcat ttttaatgtt agcagagagt acaattgtta tgatttgtta cgtctatgtg      4726

ctcaacag aca agg ctc gag gga tta tct tcg atc aag gcc gga cag tta     4776
           Thr Arg Leu Glu Gly Leu Ser Ser Ile Lys Ala Gly Gln Leu
               375                 380                 385
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gct gtt gtg ata gag gtaattattg cttgttgtga ttgtaatata agtttgcttt          4831
Ala Val Val Ile Glu
                390

gcttcagttt aagggtatct agcaaattga aattaaccta catgcag att tac gag          4887
                                                     Ile Tyr Glu

gtg gca cca tcg ctt ttc atg gta gac gta aga aag gct gct ggt gaa          4935
Val Ala Pro Ser Leu Phe Met Val Asp Val Arg Lys Ala Ala Gly Glu
     395                     400                 405

act ctt gaa tat cac aag gtttataaat atatatccaa taacaatagt                 4983
Thr Leu Glu Tyr His Lys
410                 415

ttgcatcatta ctgtgttgcg gattagagtg atattttgtt ttgtggtatc gcag ttc        5040
                                                               Phe

tac aag aag cta tgt tcg aaa ctg gaa aac ata ata tgg agg gca aca         5088
Tyr Lys Lys Leu Cys Ser Lys Leu Glu Asn Ile Ile Trp Arg Ala Thr
             420             425                 430

gaa gga ata cca aag tca gag att ctc aga aca atc acg ttt                 5130
Glu Gly Ile Pro Lys Ser Glu Ile Leu Arg Thr Ile Thr Phe
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Thr Gly Asp Asn Val Ala Ile Lys Ile Met Ala Lys Ser Thr Ile Leu
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Lys Asn Arg Met Val Asp Gln Ile Lys Arg Glu Ile Ser Ile Met Lys
50                      55                  60

Ile Val Arg His Pro Asn Ile Val Arg Leu Tyr Glu Val Leu Ala Ser
65                      70                  75                  80

Pro Ser Lys Ile Tyr Ile Val Leu Glu Phe Val Thr Gly Gly Glu Leu
                    85                  90                  95

Phe Asp Arg Ile Val His Lys Gly Arg Leu Glu Glu Ser Glu Ser Arg
                100                 105                 110

Lys Tyr Phe Gln Gln Leu Val Asp Ala Val Ala His Cys His Cys Lys
            115                 120                 125

Gly Val Tyr His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Thr
    130                 135                 140

Asn Gly Asn Leu Lys Val Ser Asp Phe Gly Leu Ser Ala Leu Pro Gln
145                 150                 155                 160

Glu Gly Val Glu Leu Leu Arg Thr Thr Cys Gly Thr Pro Asn Tyr Val
                165                 170                 175

Ala Pro Glu Val Leu Ser Gly Gln Gly Tyr Asp Gly Ser Ala Ala Asp
                180                 185                 190

Ile Trp Ser Cys Gly Val Ile Leu Phe Val Ile Leu Ala Gly Tyr Leu
            195                 200                 205

Pro Phe Ser Glu Thr Asp Leu Pro Gly Leu Tyr Arg Lys Ile Asn Ala
    210                 215                 220

Ala Glu Phe Ser Cys Pro Pro Trp Phe Ser Ala Glu Val Lys Phe Leu
225                 230                 235                 240

Ile His Arg Ile Leu Asp Pro Asn Pro Lys Thr Arg Ile Gln Ile Gln

-10-

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                245                     250                       255

Gly Ile Lys Lys Asp Pro Trp Phe Arg Leu Asn Tyr Val Pro Ile Arg
            260             265                 270

Ala Arg Glu Glu Glu Glu Val Asn Leu Asp Asp Ile Arg Ala Val Phe
        275             280             285

Asp Gly Ile Glu Gly Ser Tyr Val Ala Glu Asn Val Glu Arg Asn Asp
    290             295             300

Glu Gly Pro Leu Met Met Asn Ala Phe Glu Met Ile Thr Leu Ser Gln
305             310             315                 320

Gly Leu Asn Leu Ser Ala Leu Phe Asp Arg Arg Gln Asp Phe Val Lys
            325             330             335

Arg Gln Thr Arg Phe Val Ser Arg Arg Glu Pro Ser Glu Ile Ile Ala
            340             345             350

Asn Ile Glu Ala Val Ala Asn Ser Met Gly Phe Lys Ser His Thr Arg
        355             360             365

Asn Phe Lys Thr Arg Leu Glu Gly Leu Ser Ser Ile Lys Ala Gly Gln
    370             375             380

Leu Ala Val Val Ile Glu Ile Tyr Glu Val Ala Pro Ser Leu Phe Met
385             390             395                 400

Val Asp Val Arg Lys Ala Ala Gly Glu Thr Leu Glu Tyr His Lys Phe
            405             410             415

Tyr Lys Lys Leu Cys Ser Lys Leu Glu Asn Ile Ile Trp Arg Ala Thr
            420             425             430

Glu Gly Ile Pro Lys Ser Glu Ile Leu Arg Thr Ile Thr Phe
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            35                  40                  45


Gly Ala His Ile Gly Asn Tyr Gln Ile Val Lys Thr Leu Gly Glu Gly
        50                  55                  60


Ser Phe Gly Lys Val Lys Leu Ala Tyr His Thr Thr Thr Gly Gln Lys
65                  70                  75                  80


Val Ala Leu Lys Ile Ile Asn Lys Lys Val Leu Ala Lys Ser Asp Met
                85                  90                  95


Gln Gly Arg Ile Glu Arg Glu Ile Ser Tyr Leu Arg Leu Leu Arg His
            100                 105                 110


Pro His Ile Ile Lys Leu Tyr Asp Val Ile Lys Ser Lys Asp Glu Ile
        115                 120                 125


Ile Met Val Ile Glu Tyr Ala Gly Asn Glu Leu Phe Asp Tyr Ile Val
    130                 135                 140


Gln Arg Asp Lys Met Ser Glu Gln Glu Ala Arg Arg Phe Phe Gln Gln
145                 150                 155                 160


Ile Ile Ser Ala Val Glu Tyr Cys His Arg His Lys Ile Val His Arg
                165                 170                 175

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Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu His Leu Asn Val Lys
            180                   185             190

Ile Ala Asp Phe Gly Leu Ser Asn Ile Met Thr Asp Gly Asn Phe Leu
            195             200             205

Lys Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser
    210                 215             220

Gly Lys Leu Tyr Ala Gly Pro Glu Val Asp Val Trp Ser Cys Gly Val
225                 230             235                     240

Ile Leu Tyr Val Met Leu Cys Arg Arg Leu Pro Phe Asp Asp Glu Ser
                245             250                     255

Ile Pro Val Leu Phe Lys Asn Ile Ser Asn Gly Val Tyr Thr Leu Pro
            260             265             270

Lys Phe Leu Ser Pro Gly Ala Ala Gly Leu Ile Lys Arg Met Leu Ile
        275             280             285

Val Asn Pro Leu Asn Arg Ile Ser Ile His Glu Ile Met Gln Asp Asp
    290                 295             300

Trp Phe Lys Val Asp Leu Pro Glu Tyr Leu Leu Pro Pro Asp Leu Lys
305                 310             315                     320

Pro His Pro Glu Glu Glu Asn Glu Asn Asn Asp Ser Lys Lys Asp Gly
                325             330             335

Ser Ser Pro Asp Asn Asp Glu Ile Asp Asp Asn Leu Val Asn Ile Leu
            340             345             350

Ser Ser Thr Met Gly Tyr Glu Lys Asp Glu Ile Tyr Glu Ser Leu Glu
            355             360             365

Ser Ser Glu Asp Thr Pro Ala Phe Asn Glu Ile Arg Asp Ala Tyr Met
370                 375             380
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Leu Ile Lys Glu Asn Lys Ser Leu Ile Lys Asp Met Lys Ala Asn Lys
385             390             395             400

Ser Val Ser Asp Glu Leu Asp Thr Phe Leu Ser Gln Ser Pro Pro Thr
                405             410             415

Phe Gln Gln Gln Ser Lys Ser His Gln Lys Ser Gln Val Asp His Glu
            420             425             430

Thr Ala Lys Gln His Ala Arg Arg Met Ala Ser Ala Ile Thr Gln Gln
        435             440             445

Arg Thr Tyr His Gln Ser Pro Phe Met Asp Gln Tyr Lys Glu Glu Asp
    450             455             460

Ser Thr Val Ser Ile Leu Pro Thr Ser Leu Pro Gln Ile His Arg Ala
465             470             475             480

Asn Met Leu Ala Gln Gly Ser Pro Ala Ala Ser Lys Ile Ser Pro Leu
            485             490             495

Val Thr Lys Lys Ser Lys Thr Arg Trp His Phe Gly Ile Arg Ser Arg
        500             505             510

Ser Tyr Pro Leu Asp Val Met Gly Glu Ile Tyr Ile Ala Leu Lys Asn
    515             520             525

Leu Gly Ala Glu Trp Ala Lys Pro Ser Glu Glu Asp Leu Trp Thr Ile
    530             535             540

Lys Leu Arg Trp Lys Tyr Asp Ile Gly Asn Lys Thr Asn Thr Asn Glu
545             550             555             560

Lys Ile Pro Asp Leu Met Lys Met Val Ile Gln Leu Phe Gln Ile Glu
            565             570             575

Thr Asn Asn Tyr Leu Val Asp Phe Lys Phe Asp Gly Trp Glu Ser Ser
            580             585             590
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Tyr Gly Asp Asp Thr Thr Val Ser Asn Ile Ser Glu Asp Glu Met Ser
        595             600             605

Thr Phe Ser Ala Tyr Pro Phe Leu His Leu Thr Thr Lys Leu Ile Met
    610             615             620

Glu Leu Ala Val Asn Ser Gln Ser Asn
625             630
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<212> PRT

<213> Homo sapiens

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Val Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val Lys Ile
            20              25              30

Gly Glu His Gln Leu Thr Gly His Lys Val Ala Val Lys Ile Leu Asn
        35              40              45

Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Lys Arg Glu
    50              55              60

Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys Leu Tyr
65              70              75              80

Gln Val Ile Ser Thr Pro Thr Asp Phe Phe Met Val Met Glu Tyr Val
            85              90              95

Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys His Gly Arg Val Glu
            100             105             110
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Glu Met Glu Ala Arg Arg Leu Phe Gln Gln Ile Leu Ser Ala Val Asp
        115                 120                 125

Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro Glu Asn
        130                 135                 140

Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe Gly Leu
145                 150                 155                 160

Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly Ser
                165                 170                 175

Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr Ala Gly
                180                 185                 190

Pro Glu Val Asp Ile Trp Ser Cys Gly Val Ile Leu Tyr Ala Leu Leu
        195                 200                 205

Cys Gly Thr Leu Pro Phe Asp Asp Glu His Val Pro Thr Leu Phe Lys
        210                 215                 220

Lys Ile Arg Gly Gly Val Phe Tyr Ile Pro Glu Tyr Leu Asn Arg Ser
225                 230                 235                 240

Val Ala Thr Leu Leu Met His Met Leu Gln Val Asp Pro Leu Lys Arg
                245                 250                 255

Ala Thr Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln Gly Leu
                260                 265                 270

Pro Ser Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Asp Ala Asn Val Ile
        275                 280                 285

Asp Asp Glu Ala Val Lys Glu Val Cys Glu Lys Phe Glu Cys Thr Glu
        290                 295                 300

Ser Glu Val Met Asn Ser Leu Tyr Ser Gly Asp Pro Gln Asp Gln Leu
305                 310                 315                 320

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Ala Val Ala Tyr His Leu Ile Ile Asp Asn Arg Arg Ile Met Asn Gln
            325                 330                 335

Ala Ser Glu Phe Tyr Leu Ala Ser Ser Pro Pro Ser Gly Ser Phe Met
            340                 345                 350

Asp Asp Ser Ala Met His Ile Pro Pro Gly Leu Lys Pro His Pro Glu
            355                 360                 365

Arg Met Pro Pro Leu Ile Ala Asp Ser Pro Lys Ala Arg Cys Pro Leu
    370                 375                 380

Asp Ala Leu Asn Thr Thr Lys Pro Lys Ser Leu Ala Val Lys Lys Ala
385                 390                 395                 400

Lys Trp His Leu Gly Ile Arg Ser Gln Ser Lys Pro Tyr Asp Ile Met
                405                 410                 415

Ala Glu Val Tyr Arg Ala Met Lys Gln Leu Asp Phe Glu Trp Lys Val
            420                 425                 430

Val Asn Ala Tyr His Leu Arg Val Arg Arg Lys Asn Pro Val Thr Gly
        435                 440                 445

Asn Tyr Val Lys Met Ser Leu Gln Leu Tyr Leu Val Asp Asn Arg Ser
    450                 455                 460

Tyr Leu Leu Asp Phe Lys Ser Ile Asp Asp Glu Val Val Glu Gln Arg
465                 470                 475                 480

Ser Gly Ser Ser Thr Pro Gln Arg Ser Cys Ser Ala Ala Gly Leu His
                485                 490                 495

Arg Pro Arg Ser Ser Phe Asp Ser Thr Thr Ala Glu Ser His Ser Leu
            500                 505                 510

Ser Gly Ser Leu Thr Gly Ser Leu Thr Gly Ser Thr Leu Ser Ser Val
            515                 520                 525
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Ser Pro Arg Leu Gly Ser His Thr Met Asp Phe Phe Glu Met Cys Ala
    530                 535             540

Ser Leu Ile Thr Thr Leu Ala Arg
545                 550

<210> 5

<211> 496

<212> PRT

<213> Schizosaccharomyces pombe

<400> 5

Met Ala Gln Lys Leu Asp Asn Phe Pro Tyr His Ile Gly Arg Glu Ile
                5               10              15

Gly Thr Gly Ala Phe Ala Ser Val Arg Leu Cys Tyr Asp Asp Asn Ala
            20              25              30

Lys Ile Tyr Ala Val Lys Phe Val Asn Lys Lys His Ala Thr Ser Cys
        35              40              45

Met Asn Ala Gly Val Trp Ala Arg Arg Met Ala Ser Glu Ile Gln Leu
    50              55              60

His Lys Leu Cys Asn Gly His Lys Asn Ile Ile His Phe Tyr Asn Thr
65                  70              75                  80

Ala Glu Asn Pro Gln Trp Arg Trp Val Val Leu Glu Phe Ala Gln Gly
                85              90                  95

Gly Asp Leu Phe Asp Lys Ile Glu Pro Asp Val Gly Ile Asp Glu Asp
            100             105             110

Val Ala Gln Phe Tyr Phe Ala Gln Leu Met Glu Gly Ile Ser Phe Met
        115             120             125

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His Ser Lys Gly Val Ala His Arg Asp Leu Lys Pro Glu Asn Ile Leu
130                     135                     140

Leu Asp Tyr Asn Gly Asn Leu Lys Ile Ser Asp Phe Gly Phe Ala Ser
145                     150                     155                     160

Leu Phe Ser Tyr Lys Gly Lys Ser Arg Leu Leu Asn Ser Pro Val Gly
                165                     170                     175

Ser Pro Pro Tyr Ala Ala Pro Glu Ile Thr Gln Gln Tyr Asp Gly Ser
                180                     185                     190

Lys Val Asp Val Trp Ser Cys Gly Ile Ile Leu Phe Ala Leu Leu Leu
                195                     200                     205

Gly Asn Thr Pro Trp Asp Glu Ala Ile Ser Asn Thr Gly Asp Tyr Leu
    210                     215                     220

Leu Tyr Lys Lys Gln Cys Glu Arg Pro Ser Tyr His Pro Trp Asn Leu
225                     230                     235                     240

Leu Ser Pro Gly Ala Tyr Ser Ile Ile Thr Gly Met Leu Arg Ser Asp
                245                     250                     255

Pro Phe Lys Arg Tyr Ser Val Lys His Val Val Gln His Pro Trp Leu
                260                     265                     270

Thr Ser Ser Thr Pro Phe Arg Thr Lys Asn Gly Asn Cys Ala Asp Pro
    275                     280                     285

Val Ala Leu Ala Ser Arg Leu Met Leu Lys Leu Arg Ile Asp Leu Asp
    290                     295                     300

Lys Pro Arg Leu Ala Ser Ser Arg Ala Ser Gln Asn Asp Ser Gly Phe
305                     310                     315                     320

Ser Met Thr Gln Pro Ala Phe Lys Lys Asn Asp Gln Lys Glu Leu Asp
                325                     330                     335

Arg Val Glu Val Tyr Gly Ala Leu Ser Gln Pro Val Gln Leu Asn Lys
        340                 345                 350

Asn Ile Asp Val Thr Glu Ile Leu Glu Lys Asp Pro Ser Leu Ser Gln
        355                 360                 365

Phe Cys Glu Asn Glu Gly Phe Ile Lys Arg Leu Ala Lys Lys Ala Lys
    370                 375                 380

Asn Phe Tyr Glu Ile Cys Pro Pro Glu Arg Leu Thr Arg Phe Tyr Ser
385                 390                 395                 400

Arg Ala Ser Arg Glu Thr Ile Ile Asp His Leu Tyr Asp Ser Leu Arg
                405                 410                 415

Leu Leu Ala Ile Ser Val Thr Met Lys Tyr Val Arg Asn Gln Thr Ile
                420                 425                 430

Leu Tyr Val Asn Leu His Asp Lys Arg Lys Cys Leu Leu Gln Gly Val
        435                 440                 445

Ile Glu Leu Thr Asn Leu Gly His Asn Leu Glu Leu Ile Asn Phe Ile
    450                 455                 460

Lys Arg Asn Gly Asp Pro Leu Glu Trp Arg Lys Phe Phe Lys Asn Val
465                 470                 475                 480

Val Ser Ser Ile Gly Lys Pro Ile Val Leu Thr Asp Val Ser Gln Asn
                485                 490                 495


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<211>  476

<212>  PRT

<213>  Homo sapiens


<400>  6

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Met Ala Val Pro Phe Val Glu Asp Trp Asp Leu Val Gln Thr Leu Gly
1               5                   10                  15

Glu Gly Ala Tyr Gly Glu Val Gln Leu Ala Val Asn Arg Val Thr Glu
            20              25                  30

Glu Ala Val Ala Val Lys Ile Val Asp Met Lys Arg Ala Val Asp Cys
        35              40                  45

Pro Glu Asn Ile Lys Lys Glu Ile Cys Ile Asn Lys Met Leu Asn His
    50              55                  60

Glu Asn Val Val Lys Phe Tyr Gly His Arg Arg Glu Gly Asn Ile Gln
65                  70                  75                  80

Tyr Leu Phe Leu Glu Tyr Cys Ser Gly Gly Glu Leu Phe Asp Arg Ile
            85                  90                  95

Glu Pro Asp Ile Gly Met Pro Glu Pro Asp Ala Gln Arg Phe Phe His
            100             105                 110

Gln Leu Met Ala Gly Val Val Tyr Leu His Gly Ile Gly Ile Thr His
            115             120                 125

Arg Asp Ile Lys Pro Glu Asn Leu Leu Leu Asp Glu Arg Asp Asn Leu
    130             135                 140

Lys Ile Ser Asp Phe Gly Leu Ala Thr Val Phe Arg Tyr Asn Asn Arg
145                 150                 155                 160

Glu Arg Leu Leu Asn Lys Met Cys Gly Thr Leu Pro Tyr Val Ala Pro
            165                 170                 175

Glu Leu Leu Lys Arg Arg Glu Phe His Ala Glu Pro Val Asp Val Trp
            180             185                 190

Ser Cys Gly Ile Val Leu Thr Ala Met Leu Ala Gly Glu Leu Pro Trp
            195                 200                 205
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Asp Gln Pro Ser Asp Ser Cys Gln Glu Tyr Ser Asp Trp Lys Glu Lys
    210             215             220

Lys Thr Tyr Leu Asn Pro Trp Lys Lys Ile Asp Ser Ala Pro Leu Ala
225             230             235             240

Leu Leu His Lys Ile Leu Val Glu Asn Pro Ser Ala Arg Ile Thr Ile
            245             250             255

Pro Asp Ile Lys Lys Asp Arg Trp Tyr Asn Lys Pro Leu Lys Lys Gly
            260             265             270

Ala Lys Arg Pro Arg Val Thr Ser Gly Gly Val Ser Glu Ser Pro Ser
        275             280             285

Gly Phe Ser Lys His Ile Gln Ser Asn Leu Asp Phe Ser Pro Val Asn
    290             295             300

Ser Ala Ser Ser Glu Glu Asn Val Lys Tyr Ser Ser Ser Gln Pro Glu
305             310             315             320

Pro Arg Thr Gly Leu Ser Leu Trp Asp Thr Ser Pro Ser Tyr Ile Asp
            325             330             335

Lys Leu Val Gln Gly Ile Ser Phe Ser Gln Pro Thr Cys Pro Asp His
            340             345             350

Met Leu Leu Asn Ser Gln Leu Leu Gly Thr Pro Gly Ser Ser Gln Asn
        355             360             365

Pro Trp Gln Arg Leu Val Lys Arg Met Thr Arg Phe Phe Thr Lys Leu
    370             375             380

Asp Ala Asp Lys Ser Tyr Gln Cys Leu Lys Glu Thr Cys Glu Lys Leu
385             390             395             400

Gly Tyr Gln Trp Lys Lys Ser Cys Met Asn Gln Val Thr Ile Ser Thr
            405             410             415
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Thr Asp Arg Arg Asn Asn Lys Leu Ile Phe Lys Val Asn Leu Leu Glu
        420                 425                 430

Met Asp Asp Lys Ile Leu Val Asp Phe Arg Leu Ser Lys Gly Asp Gly
        435                 440                 445

Leu Glu Phe Lys Arg His Phe Leu Lys Ile Lys Gly Lys Leu Ile Asp
    450                 455                 460

Ile Val Ser Ser Gln Lys Val Trp Leu Pro Ala Thr
465                 470                 475
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<210> 7

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

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<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence


<220>

<223> Synthetic DNA

<400> 8
attgtactct tagccataat gttgatggct                                          30

<210> 9

<211> 38

<212> DNA

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<223> Synthetic DNA

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gcgaattctt aagttgggat caaaacgtga ttgttctg                                    38


<210> 10

<211> 30

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<400> 10
gtgataatgt agccatcaac attatggcta                                            30


<210> 11

<211> 35

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<220>

<223> Synthetic DNA

<400> 11
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<210> 12

<211> 30

<212> DNA

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<220>

<223> Synthetic DNA

<400> 12
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<210> 13

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<212> DNA

<213> Artificial Sequence


<220>

<223> Synthetic DNA

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<210> 14

<211> 38

<212> DNA

<213> Artificial Sequence


<220>

<223> Synthetic DNA

<400> 14

gcgaattctt aagttgggat caaaacgtga ttgttctg                                    38


<210>    15

<211>    35

<212>    DNA

<213>    Artificial Sequence


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<223>    Synthetic DNA

<400>    15
gcggatccat gacaaagaaa atgagaagag tgggc                                       35


<210>    16

<211>    38

<212>    DNA

<213>    Artificial Sequence


<220>

<223>    Synthetic DNA

<400>    16
gcgaattctt aagttgggat caaaacgtga ttgttctg                                    38